

Amendment to the Claims

This listing of claims will replace all prior versions and listings of claims in the above-referenced application. In accordance with 37 C.F.R. 1.121, as revised June 30, 2003, claims are labeled as “Original”, “Currently amended”, “Canceled”, “Withdrawn”, “Previously presented”, “New”, or “Not entered”.

Support for newly added claims 25-32 can be found on pages 23-29 of the specification.

Support for newly added claims 33-35 can be found on page 6 of the specification.

1. (Currently amended) A method of synthesizing an unstructured nucleic acid, the method comprising steps of:

providing a nucleic acid template strand including a first template sequence element and a second template sequence element that is substantially complementary to the first template sequence element;

providing a collection of ~~nucleotide precursors~~ nucleotides sufficient to synthesize a nucleic acid strand complementary to at least a portion of the template nucleic acid strand, which portion includes the first and second template sequence elements, the collection including ~~first and second complementary nucleotides, wherein the first and second complementary nucleotides~~ at least a first complementary nucleotide that hybridizes with a first residue within the first sequence element on the template strand and a second complementary nucleotide that hybridizes with a second residue within the second sequence element on the template strand, wherein the first and second residues are complementary to one another but the first and second nucleotides have a reduced ability to form a stable hydrogen bonded base pair an intramolecular base pair but can form an intermolecular base pair; and

contacting the template and the nucleotides with an RNA polymerase enzyme characterized by an ability to polymerize the nucleotides under conditions and for a time sufficient ~~for incorporation of the nucleotides to synthesize the~~ an unstructured nucleic acid so ~~that in which~~ said first complementary sequence element nucleotide and said second complementary sequence element nucleotide of the unstructured nucleic acid do not ~~interact with one another~~ form an intramolecular base pair.

2-9. (Canceled)

10-18. (Withdrawn)

19-24. (Canceled)

25. (New) The method of claim 1, wherein said first residue within said first sequence element on the template strand is adenine and said second residue within said second sequence element on the template strand is thymidine;

and wherein said first complementary nucleotide is 2-thiothymidine 5'-triphosphate and said second complementary nucleotide is 2-amino-2'-deoxyadenosine 5'-triphosphate.

26. (New) The method of claim 1, wherein said first residue within said first sequence element on the template strand is adenine and said second residue within said second sequence element on the template strand is uridine;

and wherein said first complementary nucleotide is 2-thiothymidine 5'-triphosphate and said second complementary nucleotide is 2-amino-2'-deoxyadenosine 5'-triphosphate.

27. (New) The method of claim 1, wherein said first residue within the first sequence element on the template strand is guanidine and said second residue within said second sequence element on the template strand is cytidine;

and wherein said first complementary nucleotide is 2'-deoxypyrrrolo-pyrimidine 5'-triphosphate and said second complementary nucleotide is 2'-deoxyinosine 5'-triphosphate.

28. (New) The method of claim 1, wherein said first residue within said first sequence element on the template strand is inosine and said second residue within said second sequence element on the template strand is cytidine;

and wherein said first complementary nucleotide is 2-thio-2'-deoxycytidine 5'-triphosphate and said second complementary nucleotide is 2'-deoxyguanosine 5'-triphosphate.

29. (New) The method of claim 1, wherein said first residue within said first sequence element on the template strand is adenine and said second residue within said second sequence element on the template strand is thymidine;

and wherein said first complementary nucleotide is 2-thiouridine 5'-triphosphate and said second complementary nucleotide is 2-aminoadenosine 5'-triphosphate.

30. (New) The method of claim 1, wherein said first residue within said first sequence element on the template strand is adenine and said second residue within said second sequence element on the template strand is uridine;

and wherein said first complementary nucleotide is 2-thiouridine 5'-triphosphate and said second complementary nucleotide is 2-aminoadenosine 5'-triphosphate.

31. (New) The method of claim 1, wherein said first residue within the first sequence element on the template strand is guanine and said second residue within said second sequence element on the template strand is cytidine;

and wherein said first complementary nucleotide is pyrrolo-pyrimidine 5'-triphosphate and said second complementary nucleotide is inosine 5'-triphosphate.

32. (New) The method of claim 1, wherein said first residue within said first sequence element on the template strand is inosine and said second residue within said second sequence element on the template strand is cytidine;

and wherein said first complementary nucleotide is 2-thiocytidine 5'-triphosphate and said second complementary nucleotide is guanosine 5'-triphosphate.

33. (New) The method of claim 1, wherein said unstructured nucleic acid is at least 40 nucleotides in length.

34. (New) The method of claim 1, wherein said unstructured nucleic acid is at least 100 nucleotides in length.

35. (New) The method of claim 1, wherein said unstructured nucleic acid is at least 500 nucleotides in length.